554 A MICROSATELLITE PHYSICAL MAP OF THE AFRICAN HUMAN MALARIA VECTOR ANOPHELES FUNESTUS. Sharakhov IV, Braginets OP, Grushko OG, Cohuet A, Guelbeogo WM, Bocollini D, Weill M, Sagnon N'F, Fontenille D, Yan G, Besansky NJ. Department of Biological Sciences, University of Notre Dame, Notre Dame, IN; Department of Biological Sciences, State University of New York at Buffalo, Buffalo, NY; Laboratoire de Lutte contre les Insectes Nuisibles, Institut de Recherche pour le Développement, Montpellier Cedex 05, France; Centre National de Recherche et de Formation sur le Paludisme, Ouagadougou, Burkina Faso; Laboratorio di Parassitologia, Istituto Superiore di Sanita, Roma, Italy; Laboratoire de Génétique et Environment, Institut des Sciences de l'Evolution, Université de Montpellier II, France.

Microsatellite markers and chromosomal inversion polymorphisms are useful genetic markers for determining population structure in Anopheline mosquitoes. In *Anopheles funestus* (2N=6), only chromosome arms 2R, 3R and 3L are known to carry polymorphic inversions. The physical location of microsatellite markers with respect to polymorphic inversions is potentially important information for interpreting population genetic structure, yet none of the available marker sets had been physically mapped in this species. Accordingly, we mapped 32 polymorphic *An. funestus* microsatellite markers to the polytene chromosomes using fluorescent in situ hybridization, and identified 16 markers outside of known polymorphic inversions. Here we provide an integrated polytene chromosome map for *An. funestus* that includes the breakpoints of all known polymorphic inversions as well as the physical locations of microsatellite loci developed to date. Based on this map, we suggest a standard set of 16 polymorphic microsatellite markers that are distributed evenly across the chromosome complement, occur predominantly outside of inversions, and amplify reliably. Adoption of this set by researchers working in different regions of Africa will facilitate metapopulation analyses of this primary malaria vector.

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